SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: DeBonte, Lorin R. Fan, Zhegong Loh, Willie H-T. Shorrosh, Basil S.
- (ii) TITLE OF THE INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fish & Richardson P.C., P.A.
 - (B) STREET: 60 South Sixth Street, Suite 3300
 - (C) CITY: Minneapolis
 - (D) STATE: MN
 - (E) COUNTRY: USA
 - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette

 - (B) COMPUTER: IBM Compatible (C) OPERATING SYSTEM: Windows95
 - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/874,109
 - (B) FILING DATE: 12-JUN-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US96/20090
 - (B) FILING DATE: 13-DEC-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Ronald C. Lundquist

 - (B) REGISTRATION NUMBER: 37,875
 - (C) REFERENCE/DOCKET NUMBER: 07148/063001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 612/335-5070
 - (B) TELEFAX: 612/288-9696 (C) TELEX:

 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Brassica napus

(ix) FEATURE:
(D) OTHER INFORMATION: Wild type Fad2.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

					AGA Arg											48
					AAG Lys											96
					AAA Lys											144
					TCC Ser											192
					GCC Ala 70		_									240
					TGG Trp											288
					GTC Val											336
					CTT Leu											384
					TAC Tyr							His			_	432
CAT His 145	Ser	AAC Asn	ACT Thr	GGC Gly	TCC Ser 150	CTC Leu	GAG Glu	AGA Arg	GAC Asp	GAA Glu 155	GTG Val	TTT Phe	GTC Val	CCC Pro	AAG Lys 160	480
					AAG Lys											528
					TTA Leu											576
					GTC Val											624

Cys		TTC Phe								672
CAG	ATA	TAC Tyr								720
		TAC Tyr								768
		CCG Pro								816
		CAC His 275							,	864
		TTC Phe								912
		AAG Lys								960
		TCC Ser								1008
		CCG Pro								1056
		GCG Ala 355								1104
		CAA Gln					Asn		T	1153
GA										1155

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 5 10 15

Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 25 30

Val\Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 50 55 60

Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240

Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 250 255

Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 275 280 285

Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 290 295 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 305 310 315 320

Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 335

Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val

. Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro

Asp\Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu

- (2) INFORMATION FOR SEQ ID NO:3:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1155 base pairs

 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Brassica napus
- (ix) FEATURE:
- (D) OTHER INFORMATION: G to A transversion mutation at nucleotide 316.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

								AAG Lys 15		48
								TTC Phe		96
								CGC Arg	TCG Ser	144
	 	 		-				GCC Ala		192
								CAC His		240
								TGC Cys 95		288
								GCC Ala		336
								CAC His		384

Phe													CGC Arg			432
CAT	TCC												GTC Val			480
													AAC Asn			528
													TGG Trp 190			576
													GGC Gly			624
													GAG Glu			672
													TAC Tyr			720
													TGC Cys			768
													ATC Ile 270			816
															TGG Trp	864
												Asp			ATC Ile	912
TTG Leu 305	AAC Asn	AAG Lys	GTC Val	TTC Phe	CAC His 310	AAT Asn	ATT Ile	ACC Thr	GAC Asp	ACG Thr 315	His	GTG Val	GCC Ala	CAT His	CAT His 320	960
										Met					GCG Ala	1008
									Gln						GTG Val	1056
													Val		CCG Pro	1104

GA

GAC AGG CAA GGT GAG AAA AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
370 . 375 380

1155

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 10 15

Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 35 40 45

Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 90 95

Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His 130 140.

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg 195 200 205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240

	Phe	Arg	Tyr	Ala	Ala 245	Gly	Gln	Gly	Val	Ala 250	Ser	Met	Val	Cys	Phe 255	Tyr	
,	Gly [\]	Wal	Pro	Leu 260	Leu	Ile	Val	Asn	Gly 265	Phe	Leu	Val	Leu	Ile 270	Thr	Tyr	
	Leu	Gln	His 275	Thr	His	Pro	Ser	Leu 280	Pro	His	Tyr	Asp	Ser 285	Ser	Glu	Trp	
	Asp	Trp 290	Phe	Arg	Gly	Ala	Leu 295	Ala	Thr	Val	Asp	Arg 300	Asp	Tyr	Gly	Ile	
	Leu 305	Asn	Lys	Val	Phe	His 310	Asn	Ile	Thr	Asp	Thr 315	His	Val	Ala	His	His 320	
	Pro	Phe	Ser	Thr	Met 325	Pro	His	Tyr	His	Ala 330	Met	Glu	Ala	Thr	Lys 335	Ala	
	Ile	Lys	Pro	Ile 340	Leu	Gly	Glu	Tyr	Tyr 345	Gln	Phe	Asp	Gly	Thr 350	Pro	Val	
	Val	Lys	Ala 355	Met	Trp	Arg	Glu	Ala 360	Lys	Glu	Cys	Ile	Tyr 365	Val	Glu	Pro	
	Asp	Arg 370	Gln	Gly	Glu	Lys	Lys 375	Gly	Val	Phe	Trp	Tyr 380	Asn	Asn	Lys	Leu	
			() () (0 (1) () ()	A) LI B) T C) S D) T LECU	CE CI ENGTI YPE: PRANI OPOLO LE TI	H: 1: nuc: DEDNI DGY: YPE:	l55 l leic ESS: line DNA	ase acio sino	pai: i	rs							
		(iv) AN	ri-s	ENSE	: NO											
		(vi			AL SO RGAN			ssic	a na	pus			•				
		(ix		ATURI D) O'	E: THER	INF	ORMA'	rion	: Wi	ld t	ype	Fad2	•				
		(xi) SE	QUEN	CE D	ESCR.	IPTI	: MC	SEQ	ID N	0:5:						
														AAA Lys		TCT Ser	48
										Cys					Phe	ACT Thr	96
				Leu					Pro					Lys		TCG Ser	144

										GAC Asp						192
										CCT Pro 75						240
										GCC Ala						288
										TGC Cys						336
										GGC Gly						384
										TAC Tyr						432
										GAA Glu 155						480
										TAC Tyr						528
										ACT Thr						576
										TAC Tyr						624
										AAC Asn		Arg				672
CAG Gln 225	ATA Ile	TAC Tyr	ATC Ile	TCC Ser	GAC Asp 230	GCT Ala	GGC Gly	ATC Ile	CTC Leu	GCC Ala 235	GTC Val	TGC Cys	TAC Tyr	GGT Gly	CTC Leu 240	720
										TCG Ser						768
										TTA Leu						816
										TAT Tyr			Ser		TGG Trp	864

	TGG Trp 290							_	ATC Ile		912
	AAC Asn										960
	TTC Phe										1008
	AAG Lys								GTG Val		1056
	AAG Lys							_			1104
	AGG Arg 370								TTA Leu	T	1153
GA											1155

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 10 15

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 25 30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 50 60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Pro His Pro 65 70 75 80

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 125 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 145 150 155 160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 195 200 205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 225 230 235 240

Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 250 255

Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 275 280 285

Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 290 295 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 305 310 315

Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 335

Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val 340 345 350

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile.Tyr Val Glu Pro 355 360 365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 370 375 380

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: YES
- (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Brassica napus

(ix) FEATURE:

(D) OTHER INFORMATION: T to A transversion mutation at nucleotide 515.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

	,		•													
						ATG Met										48
						CGC Arg								_		96
						GCA Ala										144
						TAC Tyr 55										192
						ACC Thr										240
						CCT Pro										288
						ATA Ile										336
						GAC Asp										384
						TTC Phe 135										432
															AAG Lys 160	480
															TTG Leu	528
GGA Gly	CGC Arg	ACC Thr	GTG Val 180	ATG Met	TTA Leu	ACG Thr	GTT Val	CAG Gln 185	TTC Phe	ACT Thr	CTC Leu	GGC Gly	TGG Trp 190	CCT Pro	TTG Leu	576
													Gly		GCT Ala	624

	ys													GAG Glu				672
G	'AG	ATA	TAC Tyr	ATC Ile	TCC Ser	GAC Asp 230	GCT Ala	GGC Gly	ATC Ile	CTC Leu	GCC Ala 235	GTC Val	TGC Cys	TAC Tyr	GGT Gly	CTC Leu 240		720
														TGC Cys				768
														ATC Ile 270				816
														TCT Ser				864
														TAC Tyr				912
I	TG Leu 105	AAC Asn	AAG Lys	GTC Val	TTC Phe	CAC His 310	AAT Asn	ATC Ile	ACG Thr	GAC Asp	ACG Thr 315	CAC His	GTG Val	GCG Ala	CAT His	CAC His 320		960
														ACG Thr				1008
														ACG Thr 350				1056
														GTG Val				1104
A	AC Asp	AGG Arg 370	CAA Gln	GGT Gly	GAG Glu	AAG Lys	AAA Lys 375	GGT Gly	GTG Val	TTC Phe	TGG Trp	TAC Tyr 380	Asn	AAT Asn	AAG Lys	TTA Leu	Т	1153
C	A																	1155

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 5 10 15

Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 25

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 215 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 280 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325

Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 370 375 380

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1152
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG Met 1	GGT Gly	GCA Ala	GGT Gly	GGA Gly 5	AGA Arg	ATG Met	CAA Gln	GTG Val	TCT Ser 10	CCT Pro	CCC Pro	TCC Ser	AAA Lys	AAG Lys 15	TCT Ser	48
GAA Glu	ACC Thr	GAC Asp	AAC Asn 20	ATC Ile	AAG Lys	CGC Arg	GTA Val	CCC Pro 25	TGC Cys	GAG Glu	ACA Thr	CCG Pro	CCC Pro 30	TTC Phe	ACT Thr	96
GTC Val	GGA Gly	GAA Glu 35	CTC Leu	AAG Lys	AAA Lys	GCA Ala	ATC Ile 40	CCA Pro	CCG Pro	CAC His	TGT Cys	TTC Phe 45	AAA Lys	CGC Arg	TCG Ser	144
ATC Ile	CCT Pro 50	CGC Arg	TCT Ser	TTC Phe	TCC Ser	TAC Tyr 55	CTC Leu	ATC Ile	TGG Trp	GAC Asp	ATC Ile 60	ATC Ile	ATA Ile	GCC Ala	TCC Ser	192
TGC Cys 65	TTC Phe	TAC Tyr	TAC Tyr	GTC Val	GCC Ala 70	ACC Thr	ACT Thr	TAC Tyr	TTC Phe	CCT Pro 75	CTC Leu	CTC Leu	CCT Pro	CAC His	CCT Pro 80	240
CTC Leu	TCC Ser	TAC Tyr	TTC Phe	GCC Ala 85	TGG Trp	CCT Pro	CTC Leu	TAC Tyr	TGG Trp 90	GCC Ala	TGC Cys	CAG Gln	GGC Gly	TGC Cys 95	GTC Val	288
CTA Leu	ACC Thr	GGC Gly	GTC Val 100	TGG Trp	GTC Val	ATA Ile	GCC Ala	CAC His 105	GAG Glu	TGC Cys	GGC Gly	CAC His	CAC His 110	GCC Ala	TTC Phe	336
AGC Ser	GAC Asp	TAC Tyr 115	CAG Gln	TGG Trp	CTG Leu	GAC Asp	GAC Asp 120	ACC Thr	GTC Val	GGC Gly	CTC Leu	ATC Ile 125	TTC Phe	CAC His	TCC Ser	384
TTC Phe	CTC Leu 130	CTC Leu	GTC Val	CCT Pro	TAC Tyr	TTC Phe 135	TCC Ser	TGG Trp	AAG Lys	TAC Tyr	AGT Ser 140	CAT His	CGA Arg	. CGC Arg	CAC His	432
CAT His 145	Ser	AAC Asn	ACT Thr	GGC Gly	TCC Ser 150	Leu	GAG Glu	AGA Arg	GAC Asp	GAA Glu 155	. Val	TTT Phe	GTC Val	CCC Pro	AAG Lys 160	480

	AAG Lys																528
	CGC Arg																576
	TTA Leu																624
	CAT His 210																672
	ATA Ile																720
	CGC Arg																768
	GTT Val																816
TTG Leu	CAG Gln	CAC His 275	ACG Thr	CAT His	CCT Pro	TCC Ser	CTG Leu 280	CCT Pro	CAC His	TAT Tyr	GAC Asp	TCG Ser 285	TCT Ser	GAG Glu	TGG Trp		864
	TGG Trp 290																912
	AAC Asn																960
	TTC Phe																1008
	AAG Lys																1056
	AAG Lys																1104
	AGG Arg 370											Asn			TTA Leu	Т	1153
GA																	1155

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids

 - (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Me 1	t Gly	Ala	Gly	Gly 5	Arg	Met	Gln	Val	Ser 10	Pro	Pro	Ser	Lys	Lys 15	Ser
G1	u Thr	Asp	Asn 20	Ile	Lys	Arg	Val	Pro 25	Cys	Glu	Thr	Pro	Pro 30	Phe	Thr
۷a	l Gly	Glu 35	Leu	Lys	Lys	Ala	Ile 40	Pro	Pro	His	Cys	Phe 45	Lys	Arg	Ser
Il	e Pro 50	Arg	Ser	Phe	Ser	Tyr 55	Leu	Ile	Trp	Asp	Ile 60	Ile	Ile	Ala	Ser
Су 65	s Phe	Tyr	Tyr	Val	Ala 70	Thr	Thr	Tyr	Phe	Pro 75	Leu	Leu	Pro	His	Pro 80
	ı Ser			85					90					95	
	u Thr		100					105					110		
	r Asp	115					120					125			
	e Leu 130					135					140				
14					150					155					160
	s Lys			165					170					175	
	y Arg		180					185					190		
	r Leu	195					200	_		_	_	205			
	s His 210					215			_		220				
22		-			230		-			235	•	_			240
•	r Arg	•		245			_		250					255	
	y Val		260					265					270		
	u Gln -	275					280			-	_	285			
	p Trp 290					295					300				
30	-				310					315					320
	u Phe			325					330					335	
	e Lys		340					345					350		
	l Lys	355					360					365			
AS	p Arg 370	GIN	GTÅ	GIU	ьys	175 375	GTÅ	val	rne	rrp	380	ASI	ASA	пÀр	nen

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (ix) FEATURE:
- - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1152 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

							AAG Lys 15		4	8
							TTC Phe		9	6
							CGC Arg		14	4
							GCC Ala		19	2
							CAC His		24	ŧ0
							TGC Cys 95		28	88
							GCC Ala		33	36
							CAC His		38	34
							CGC Arg		43	32
							CCC Pro	AAG Lys 160	4.8	30
							CCT Pro 175	TTG Leu	52	28

	Thr	ATG Met								576
TAC		AAC Asn								624
		CCC Pro								672
		TCC Ser								720
		GCT Ala 245								768
		CTG Leu								816
		CAT His								864
		GGA Gly								912
		TTC Phe								960
		ATG Met 325								1008
		CTG Leu								1056
		TGG Trp						CCG Pro		1104
		GAG Glu						TTA Leu	T	1153
GA										1155

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 25 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 40 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 85 90 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe 105 100 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 135 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 150 155 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 170 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 185 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 205 200 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 215 220 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 230 235 Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr 245 250 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 260 265 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 280 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 290 295 300 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 315 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val 345 350 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 365 360 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...1152
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGT Gly									48
ACC Thr									96
GGA Gly									144
CCT Pro 50									192
TTC Phe									240
TCC Ser									288
ACC Thr									336
GAC Asp						_	_	 	384
CTC Leu 130			_						432
TCC Ser									480
AAG Lys									528
								TTG Leu	576
TTA Leu								GCT Ala	624

				ATC Ile			_			672
CAG				ATC Ile						720
				GTG Val						768
				GGT Gly 265						816
				CCT Pro						864
				ACC Thr						912
				ACC Thr						960
				CAC His						1008
				TAT Tyr 345						1056
				AAG Lys						1104
				GTG Val				TTA Leu	T	1153
GA										1155

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids

 - (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 90 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 105 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 120 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 150 155 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 190 180 185 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 200 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 215 220 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 230 235 Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 260 265 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 275 280 285 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 295 300 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 310 315 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 325 330 335 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val 345 340 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 360 • 365 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 375

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1152
 - (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

			AGA Arg						48
			AAG Lys						96
			AAA Lys						144
	 	 	TCC Ser	 			_		192
			GCC Ala 70						240
			TGG Trp						288
			GTC Val						336
			CTT Leu						384
			TAC Tyr						432
			TCC Ser 150						480
			AAG Lys						528
			TTA Leu						576
			GTC Val						624
			AAC Asn						672
						Val		CTC Leu 240	720

							TTC Phe 255			768
GGA							ACT Thr			816
							GAG Glu			864
							GGA Gly			912
							CAT His			960
							AAG Lys 335	_		1008
							CCG Pro	_		1056
							GAA Glu			1104
	 	 		 	 		AAG Lys	TTA Leu	Т	1153
GA										1155

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 15 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 25 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 40 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 60 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro 70

Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 90 85 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 105 100 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 125 115 120 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 140 135 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 155 150 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr His Asn Asn Pro Leu 170 165 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 190 185 180 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 205 200 195 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 220 215 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 230 235 Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr 250 245 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 270 265 260 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 285 280 275 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile 300 295 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 315 310 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 335 330 325 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val 350 345 340 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 365 360 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 380

- (2) INFORMATION FOR SEQ ID NO:17:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1152
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 1 10 15

48

Glu	ACC Thr	Asp	ACC Thr 20	ATC Ile	AAG Lys	CGC Arg	GTA Val	CCC Pro 25	TGC Cys	GAG Glu	ACA Thr	CCG Pro	CCC Pro 30	TTC Phe	ACT Thr	96	;
GTC Val	GGA Gly	GAA Glu 35	CTC Leu	AAG Lys	AAA Lys	GCA Ala	ATC Ile 40	CCA Pro	CCG Pro	CAC His	TGT Cys	TTC Phe 45	AAA Lys	CGC Arg	TCG Ser	144	Ė
ATC Ile	CCT Pro 50	CGC Arg	TCT Ser	TTC Phe	TCC Ser	TAC Tyr 55	CTC Leu	ATC Ile	TGG Trp	GAC Asp	ATC Ile 60	ATC Ile	ATA Ile	GCC Ala	TCC Ser	192	2
TGC Cys 65	TTC Phe	TAC Tyr	TAC Tyr	GTC Val	GCC Ala 70	ACC Thr	ACT Thr	TAC Tyr	TTC Phe	CCT Pro 75	CTC Leu	CTC Leu	CCT Pro	CAC His	CCT Pro 80	240)
CTC Leu	TCC Ser	TAC Tyr	TTC Phe	GCC Ala 85	TGG Trp	CCT Pro	CTC Leu	TAC Tyr	TGG Trp 90	GCC Ala	TGC Cys	CAA Gln	GGG Gly	TGC Cys 95	GTC Val	288	3
CTA Leu	ACC Thr	GGC Gly	GTC Val 100	TGG Trp	GTC Val	ATA Ile	GCC Ala	CAC His 105	GAG Glu	TGC Cys	GGC Gly	CAC His	CAC His 110	GCC Ala	TTC Phe	336	5
AGC Ser	GAC Asp	TAC Tyr 115	CAG Gln	TGG Trp	CTT Leu	GAC Asp	GAC Asp 120	ACC Thr	GTC Val	GGT Gly	CTC Leu	ATC Ile 125	TTC Phe	CAC His	TCC Ser	384	1
TTC Phe	CTC Leu 130	CTC Leu	GTC Val	CCT Pro	TAC Tyr	TTC Phe 135	TCC Ser	TGG Trp	AAG Lys	TAC Tyr	AGT Ser 140	CAT His	CGA Arg	CGC Arg	CAC His	432	2
CAT His 145	TCC Ser	AAC Asn	ACT Thr	GGC Gly	TCC Ser 150	CTC Leu	GAG Glu	AGA Arg	GAC Asp	GAA Glu 155	Val	TTT Phe	GTC Val	CCC Pro	AAG Lys 160	480	0
AAG Lys	AAG Lys	TCA Ser	GAC Asp	ATC Ile 165	AAG Lys	TGG Trp	TAC Tyr	GGC Gly	AAG Lys 170	TAC Tyr	CTC Leu	AAC Asn	AAC Asn	CCT Pro 175	TTG Leu	52	8
GGA Gly	CGC Arg	ACC Thr	GTG Val 180	ATG Met	TTA Leu	ACG Thr	GTT Val	CAG Gln 185	TTC Phe	ACT Thr	CTC Leu	GGC Gly	TGG Trp 190	CCG Pro	TTG Leu	57	6
TAC Tyr	TTA Leu	GCC Ala 195	Phe	AAC Asn	GTC Val	TCG Ser	GGA Gly 200	Arg	CCT Pro	TAC Tyr	GAC Asp	GGC Gly 205	Gly	TTC Phe	GCT Ala	62	4
TGC Cys	CAT His 210	Phe	CAC His	CCC Pro	AAC Asn	GCT Ala 215	CCC	ATC Ile	TAC Tyr	AAC Asn	GAC Asp 220	Arg	GAG Glu	CGT Arg	CTC Leu	67	2
CAG Gln 225	Ile	TAC Tyr	ATC Ile	TCC Ser	GAC Asp 230	Ala	GGC Gly	ATC	CTC Leu	GCC Ala 235	Val	TGC Cys	TAC Tyr	GGT Gly	CTC Leu 240	72	0
TTC Phe	CGT Arg	TAC	GCC Ala	GCC Ala 245	Ala	CAG Gln	GGA Gly	GTG Val	GCC Ala 250	Ser	ATG Met	GTC Val	TGC Cys	TTC Phe 255	TAC Tyr	76	8

GGA Gly	GTC Val	Pro	CTT Leu 260	CTG Leu	ATT Ile	GTC Val	AAT Asn	GGT Gly 265	TTC Phe	CTC Leu	GTG Val	TTG Leu	ATC Ile 270	ACT Thr	TAC Tyr		816
TTG Leu	CAG Gln	CAC His 275	ACG Thr	CAT His	CCT Pro	TCC Ser	CTG Leu 280	CCT Pro	CAC His	TAC Tyr	GAT Asp	TCG Ser 285	TCC Ser	GAG Glu	TGG Trp	_	864
GAT Asp	TGG Trp 290	TTG Leu	AGG Arg	GGA Gly	GCT Ala	TTG Leu 295	GCT Ala	ACC Thr	GTT Val	GAC Asp	AGA Arg 300	GAC Asp	TAC Tyr	GAA Glu	ATC Ile		912
TTG Leu 305	AAC Asn	AAG Lys	GTC Val	TTC Phe	CAC His 310	AAT Asn	ATT Ile	ACC Thr	GAC Asp	ACG Thr 315	CAC His	GTG Val	GCG Ala	CAT His	CAT His 320		960
CTG Leu	TTC Phe	TCC Ser	ACG Thr	ATG Met 325	CCG Pro	CAT His	TAT Tyr	CAC His	GCG Ala 330	ATG Met	GAA Glu	GCT Ala	ACC Thr	AAG Lys 335	GCG Ala		1008
ATA Ile	AAG Lys	CCG Pro	ATA Ile 340	CTG Leu	GGA Gly	GAG Glu	TAT Tyr	TAT Tyr 345	CAG Gln	TTC Phe	GAT Asp	GGG Gly	ACG Thr 350	CCG Pro	GTG Val		1056
GTT Val	AAG Lys	GCG Ala 355	ATG Met	TGG Trp	AGG Arg	GAG Glu	GCG Ala 360	Lys	GAG Glu	TGT Cys	ATC Ile	TAT Tyr 365	vaı	GAA Glu	CCG Pro		1104
GAC Asp	AGG Arg 370	CAA Gln	GGT Gly	GAG Glu	AAG Lys	AAA Lys 375	GGT Gly	GTG Val	TTC Phe	TGG Trp	TAC Tyr 380	Asn	AAT Asn	AAG Lys	TTA Leu	T	1153
GA																	1155

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 384 amino acids
 (B) TYPE: amino acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 45 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val 95 90 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 105 100

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 120 115 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 135 140 ****130 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 155 150 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 170 165 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu 190 185 180 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala 200 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu 215 220 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu 230 235 Phe Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Phe Tyr 250 245 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr 265 260 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp 280 Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Glu Ile 300 295 290 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His 310 315 Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala 335 330 325 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val 345 340 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro 365 360 355 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu 380

- (2) INFORMATION FOR SEQ ID NO:19:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other Nucleic Acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGATATGATG ATGGTGAAAG A

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Other Nucleic Acid
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCTTTCACCA TCATCATATC C

21

21

	(2) INFORMATION FOR SEQ ID NO:21:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: Other Nucleic Acid	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GTTATG	BAGC AAAGAAGAAA C	21
	(2) INFORMATION FOR SEQ ID NO:22:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 26 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: Other Nucleic Acid	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
GTTTCT	TCTT TGCTTTGCTT CATAAC	26
	(2) INFORMATION FOR SEQ ID NO:23:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: Other Nucleic Acid	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
CAUCAU	JCAUC AUCTTCTTCG TAGGGTTCAT CG	32
	(2) INFORMATION FOR SEQ ID NO:24:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: Other Nucleic Acid	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
CITACIT	ACTIAC HATCATAGAA GAGAAAGGTT CAG	33

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: Genomic DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
CAUCAUCAUC AUCATGGGTG CACGTGGAAG AA	32
(2) INFORMATION FOR SEQ ID NO:26:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: Genomic DNA	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
CUACUACUAC UATCTTTCAC CATCATCATA TCC	33

(2) INFORMATION FOR SEQ ID NO:25: